

## **Cellular pathogenesis of Duchenne muscular dystrophy: progressive myofibre degeneration, chronic inflammation, reactive myofibrosis and satellite cell dysfunction**

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### **Abstract**

Duchenne muscular dystrophy is a highly progressive muscle wasting disease of early childhood and characterized by complex pathophysiological and histopathological changes in the voluntary contractile system, including myonecrosis, chronic inflammation, fat substitution and reactive myofibrosis. The continued loss of functional myofibres and replacement with non-contractile cells, as well as extensive tissue scarring and decline in tissue elasticity, leads to severe skeletal muscle weakness. In addition, dystrophic muscles exhibit a greatly diminished regenerative capacity to counteract the ongoing process of fibre degeneration. In normal muscle tissues, an abundant stem cell pool consisting of satellite cells that are localized between the sarcolemma and basal lamina, provides a rich source for the production of activated myogenic progenitor cells that are involved in efficient myofibre repair and tissue regeneration. Interestingly, the self-renewal of satellite cells for maintaining an essential pool of stem cells in matured skeletal muscles is increased in dystrophin-deficient fibres. However, satellite cell hyperplasia does not result in efficient recovery of dystrophic muscles due to impaired asymmetric cell divisions. The lack of expression of the full-length dystrophin isoform Dp427-M, which is due to primary defects in the DMD gene, appears to affect key regulators of satellite cell polarity causing a reduced differentiation of myogenic progenitors, which are essential for myofibre regeneration. This review outlines the complexity of dystrophinopathy and describes the importance of the pathophysiological role of satellite cell dysfunction. A brief discussion of the bioanalytical usefulness of single cell proteomics for future studies of satellite cell biology is provided.

**Key Words:** dystrophinopathy, fibrosis, immune response, myoblast, stem cell.

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This review on the cellular pathogenesis of Duchenne muscular dystrophy (DMD) is part of the Special Issue on ‘Muscle Satellite Cells in Health and Disease’ in the European Journal of Translational Myology, edited by Massimo Ganassi and Zipora Yablonka-Reuveni.<sup>1</sup> The quintessential satellite cell (SC) population, discovered independently in 1961 by Alexander Mauro and Bernard Katz,<sup>2-5</sup> represents resident myogenic stem cells in skeletal muscles.<sup>6-8</sup> SCs are of central importance for supporting neuromuscular homeostasis, myofiber maintenance, muscle plasticity and the high degree of adaptability of the voluntary contractile system to changed functional demands, as well as the remarkable regenerative capacity of skeletal muscles that underlie the self-repair capabilities of myofibres following

traumatic injury, chronic disease or aging-related functional decline.<sup>9-11</sup> Interestingly, during myofiber regeneration in long-term denervated muscles, the relative number of SCs remains at a high level.<sup>12,13</sup> Morphological studies have shown that the regeneration of contractile fibres plays a crucial role in the maintenance of chronically denervated skeletal muscles. Replication of SCs clearly occurs after drug-induced muscle damage, using repeated applications of the local anaesthetic and nerve blocking agent bupivacaine, even in the absence of reinnervation.<sup>12</sup>

The self-renewal of SCs is finely regulated in order to maintain an essential stem cell pool in matured skeletal muscles.<sup>7</sup> This process is balanced with the production of myogenic progenitor cells,<sup>8</sup> which are involved in

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efficient myofibre repair and regeneration.<sup>14</sup> A disturbance of this delicate balance between symmetric versus asymmetric cell division of activated SCs causes a diminished regenerative capacity and thus plays a crucial role in neuromuscular pathology.<sup>10</sup> This article focuses on the pathophysiological complexity of DMD and provides an overview of the role of SC dysfunction as a critical part of the overall damage pathway that leads to contractile weakness in dystrophic muscles.<sup>15</sup> Abnormal functioning of the resident stem cell pool in dystrophin-deficient muscle fibres appears to be of central importance for the weakened regenerative capacity of dystrophic myofibres,<sup>16-19</sup> making it an integral part of the major symptoms of dystrophinopathy, i.e. progressive skeletal muscle degeneration, fat replacement, reactive myofibrosis and chronic sterile inflammation.<sup>20-22</sup>

In this review, we outline the pathophysiological mechanisms that involve fibre necrosis, myofibrosis, a sustained immune response and SC dysfunction, and briefly outline the relevance of these destructive processes for the development and innovative design of novel therapies to treat dystrophin deficiency. For the selection of up-to-date publications to be discussed in this article on dystrophinopathy, the roles of myonecrosis, myofibrosis, inflammation and SC dysfunction were reviewed by literature screening using a combination of search terms, such as 'dystrophin', 'necrosis', 'myonecrosis', 'fibrosis', 'myofibrosis', 'inflammation', 'satellite cell', 'myoblast', 'dystrophinopathy' and 'Duchenne muscular dystrophy' in the Pubmed database. The identified list of publications was then further screened for their relevance to this review of the molecular and cellular pathogenesis of DMD.

**Dystrophinopathy**

DMD is an X-chromosomally inherited and highly progressive muscular disorder of early childhood.<sup>23</sup> Primary defects in the *DMD* gene trigger the almost complete loss of the membrane cytoskeletal protein named dystrophin.<sup>24</sup> However, a large number of promoters produce a variety of tissue-specific dystrophin protein isoforms.<sup>25</sup> Thus, depending on individual mutations within the extremely large *DMD* gene, in combination with genetic modifiers, the bodily functions of Duchenne patients can be affected in a variety of ways.<sup>26-28</sup> Besides skeletal muscle wasting, multi-systemic complications can occur, including late-onset cardio-respiratory syndrome,<sup>29</sup> neuronal abnormalities,<sup>30</sup> and dysfunction of the kidneys, bladder, liver, digestive tract and the immune system.<sup>31</sup> Here, we focus on the complexity of progressive skeletal muscle degeneration. Figure 1 outlines the promoter structure of the human *DMD* gene, the major domains of the full-length Dp427-M protein isoform of dystrophin that is expressed in myofibres, and the localization of the various components of the dystrophin-associated glycoprotein complex at the sarcolemma. The core dystrophin

complex consists of  $\alpha/\beta$ -dystroglycan,  $\alpha/\beta/\gamma/\delta$ -sarcoglycan, sarcospan,  $\alpha/\beta$ -syntrophin and  $\alpha$ -dystrobrevin.<sup>32</sup> The tight linkage between the  $\alpha/\beta$ -dystroglycan sub-complex and Dp427-M bridges the plasmalemma membrane and provides a stabilizing protein assembly between the sub-sarcolemmal actin cytoskeleton and the laminin-211 complex, which in turn binds collagen isoform COL-IV of the basal lamina.<sup>33</sup> Importantly, this indirect association between the intracellular cytoskeleton and the extracellular matrix prevents excess damage to the fibre periphery during repeated excitation-contraction-relaxation cycles or rigorous muscle stretching in normal muscle.<sup>32,34</sup>

As listed in Figure 1, the major functions of the core dystrophin complex include the provision of a trans-sarcolemmal linkage, the stabilization of the myofibre periphery, the organization of the intracellular network of cytoskeletal elements, the facilitation of a sarcolemmal signalling hub and the mechanical support for lateral force transmission at costamere structures.<sup>34</sup> Hence, a better understanding of the loss of dystrophin-associated proteins due to dystrophin deficiency and their involvement in the molecular and cellular pathogenesis of dystrophinopathy is critical for the identification of novel therapeutic targets and the development of new strategies to treat X-linked muscular dystrophy, such as improved pharmacological interventions, stem cell therapy and/or gene therapy.<sup>35-38</sup> Furthermore, biomarker discovery is of central importance for the improved diagnosis, prognosis and therapeutic monitoring of DMD.<sup>39-41</sup>

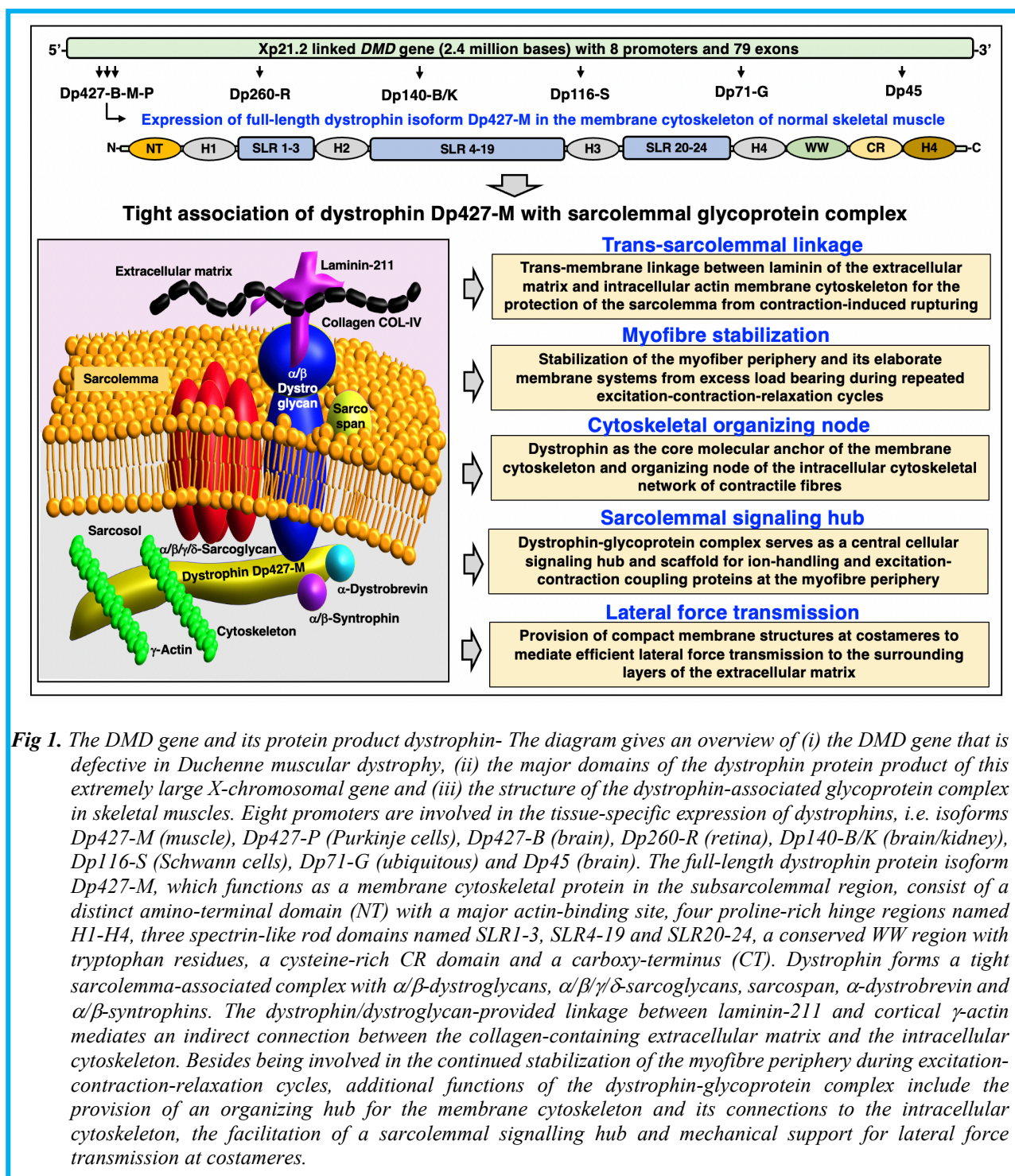
**Chronic myofibre degeneration**

Myonecrosis is the pathophysiological initiator of the complex degenerative processes that occur in dystrophic muscle fibres.<sup>22,23</sup> The absence of dystrophin partially eliminates the molecular anchoring capacity of the sarcolemma and thereby causes the loss of the dystrophin-associated glycoprotein complex.<sup>42-44</sup> The reduced expression of dystroglycans, sarcoglycans, dystrobrevins, syntrophins and sarcospan triggers impaired sarcolemmal integrity due to the loss of the linkage between laminin-211 and cortical  $\gamma$ -actin.<sup>33</sup> Weakened costameres result in diminished lateral force transmission and lessened load bearing capacity. Contraction-induced micro-rupturing of the surface membrane system damages the cellular unity of the muscular system. Sarcolemmal disintegration,<sup>45</sup> was shown to be directly linked to a calcium-dependent damage pathway in X-linked muscular dystrophy.<sup>46</sup>  $\text{Ca}^{2+}$ -ions flux through the disrupted plasmalemma and  $\text{Ca}^{2+}$ -leak channels, which causes chronically elevated  $\text{Ca}^{2+}$ -levels in the sarcosol. In conjunction with impaired luminal  $\text{Ca}^{2+}$ -buffering,<sup>47,48</sup> this triggers  $\text{Ca}^{2+}$ -dependent proteolysis leading to myofiber degradation,<sup>49</sup> as summarized in Figure 2.

The systematic analysis of dystrophic animal models, such as dystrophin-lacking mice, dogs or pigs,<sup>50-52</sup> was

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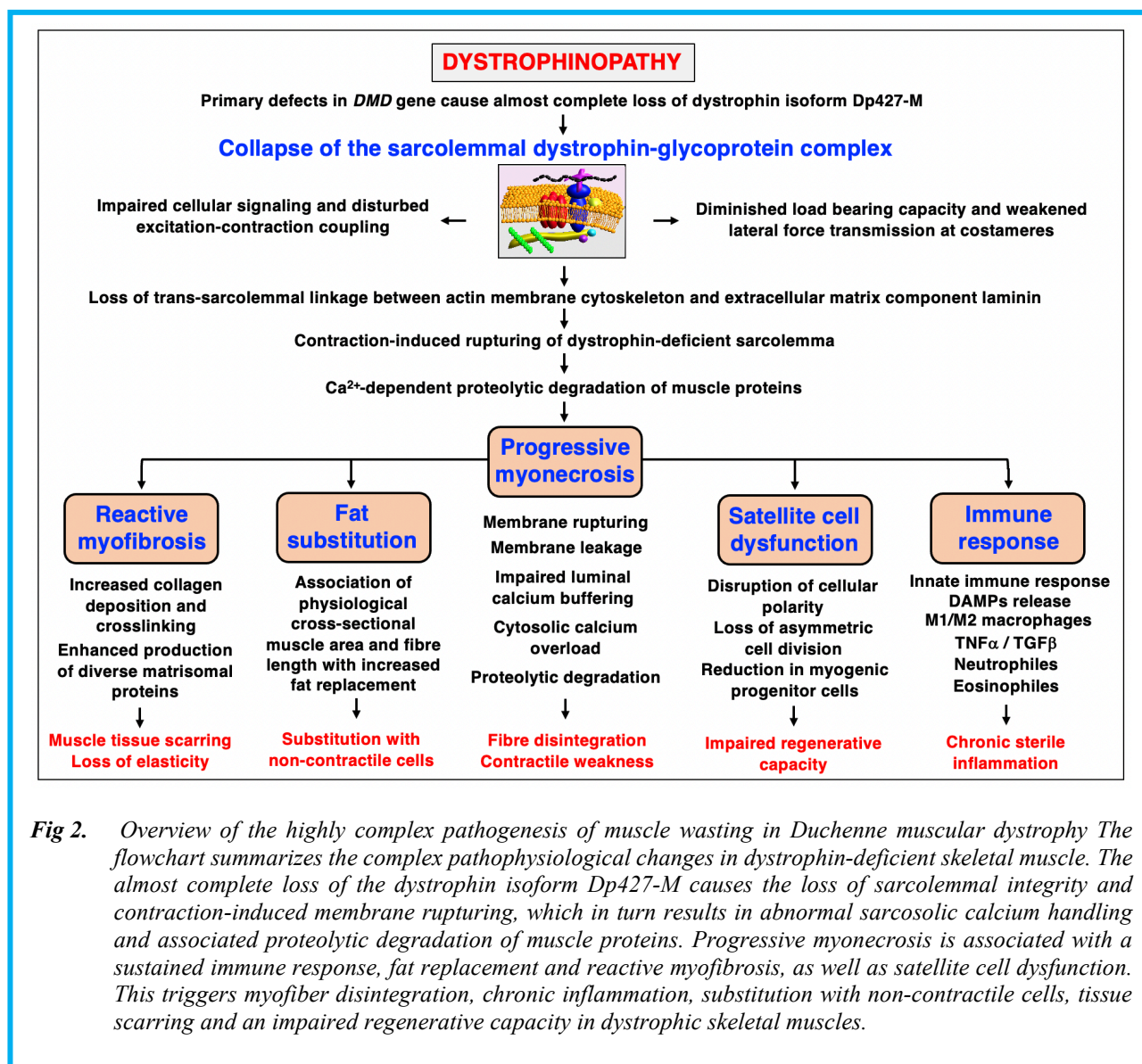
crucial for the elucidation of myonecrosis and associated degenerative processes in muscular dystrophy.<sup>53,54</sup> Various *mdx*-type mouse models are frequently used for biomarker discovery, the identification of novel therapeutic targets and the testing of experimental treatments.<sup>55-57</sup> Proteome-wide alterations in dystrophin-deficient muscle specimens were shown to include characteristic abundance changes in proteins involved in excitation-contraction coupling, the contraction-

relaxation cycle, ion homeostasis, bioenergetic pathways, the cellular stress response, the cytoskeleton, signalling cascades, membrane repair, and the extracellular matrix.<sup>49,57</sup>

The diagram in Figure 2 gives an overview of the complexity of dystrophinopathy, including the pathophysiological role of tissue scarring, loss of muscle elasticity, substitution with non-contractile cells, impairment of the regenerative capacity of dystrophic

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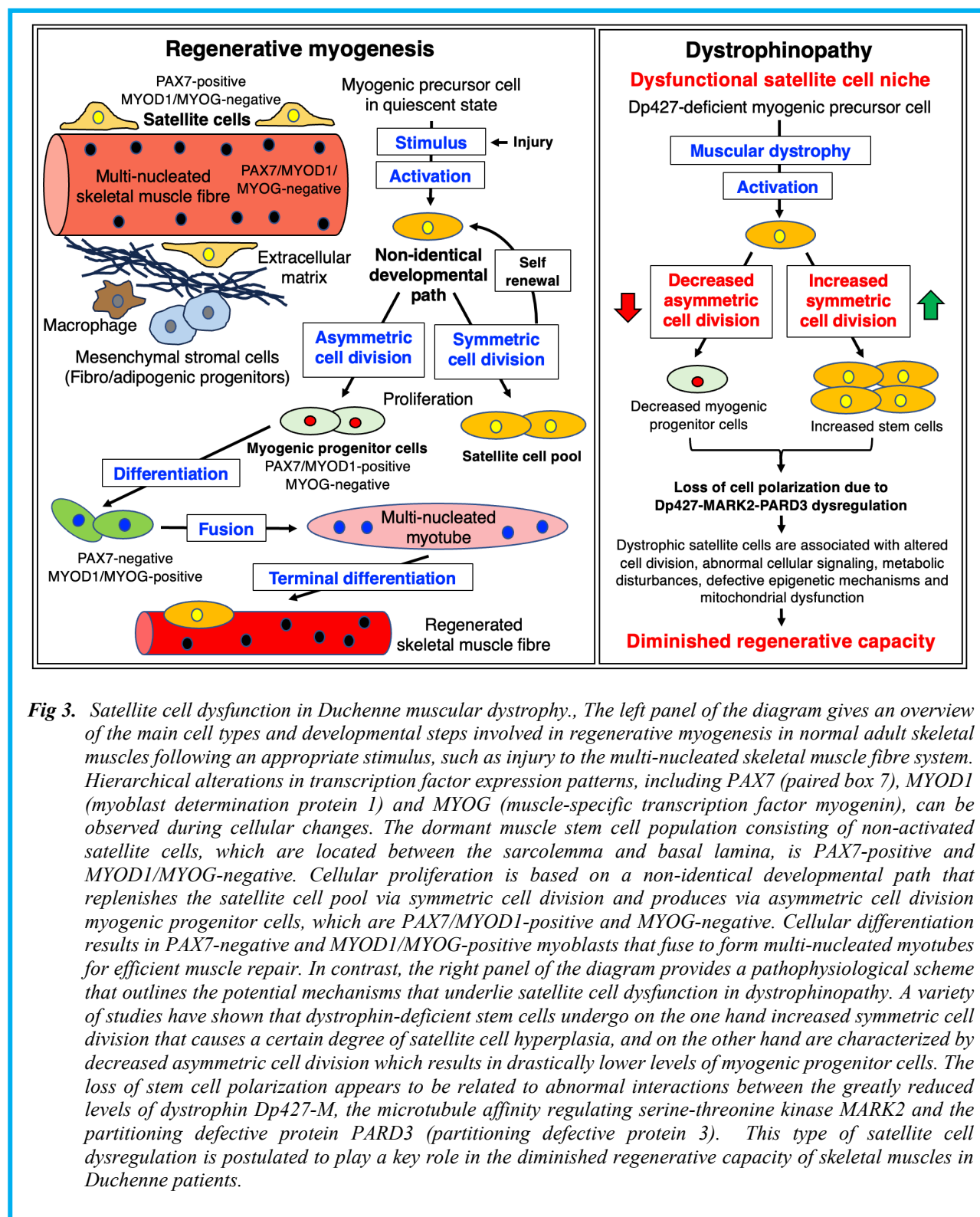
**Fig 2.** Overview of the highly complex pathogenesis of muscle wasting in Duchenne muscular dystrophy. The flowchart summarizes the complex pathophysiological changes in dystrophin-deficient skeletal muscle. The almost complete loss of the dystrophin isoform Dp427-M causes the loss of sarcolemmal integrity and contraction-induced membrane rupturing, which in turn results in abnormal sarcosolic calcium handling and associated proteolytic degradation of muscle proteins. Progressive myonecrosis is associated with a sustained immune response, fat replacement and reactive myofibrosis, as well as satellite cell dysfunction. This triggers myofiber disintegration, chronic inflammation, substitution with non-contractile cells, tissue scarring and an impaired regenerative capacity in dystrophic skeletal muscles.

muscles and chronic sterile inflammation.<sup>58</sup> These changes in muscle integrity are related to exacerbated immune responses, fibre necrosis, fat replacement, reactive myofibrosis and SC dysfunction,<sup>59</sup> as described in below sections.

### Chronic sterile inflammation

In DMD, a sustained immune response can be observed as a reaction to progressive fibre necrosis,<sup>20</sup> involving initially mostly the innate immune system.<sup>60</sup> However, crosstalk signalling exists between the innate immune response and T-cell adaptive immunity within the skeletal muscular system.<sup>61,62</sup> Within the lymphatic system, striking morphological changes were shown to occur in lymph nodes in association with muscular dystrophy. This affects especially the white pulp region of the spleen. In the dystrophic organism, the abundance of splenic inflammatory monocytes changes and immune cells migrate at an elevated rate from their splenic

reservoir to dystrophin-deficient myofibres.<sup>63</sup> The systematic and mass spectrometry-based proteomic screening of spleen specimens from the *mdx-4cv* mouse model of dystrophinopathy confirmed this crosstalk between lymphoid organs and dystrophic skeletal muscles.<sup>64,65</sup> Splenic monocyte transfer to damaged myofibres and their subsequent differentiation into macrophages is a crucial underlying factor for chronic inflammation in muscular dystrophy.<sup>66</sup> Prolonged M1 and M2 macrophage activity,<sup>67</sup> based on both resident macrophages and infiltrating myocytes, and cytokine release are associated with a chronic inflammatory state of dystrophic fibres.<sup>68</sup> The massive infiltration of dystrophic fibres by macrophages, neutrophils and dendritic cell populations is mediated by extensive cytokine and chemokine signalling events.<sup>59,62</sup> The transforming growth factor TGF- $\beta$  is released from M2 macrophages and initiates the activation of stromal cells that can adapt to multiple cellular lineages,<sup>69</sup>



**Fig 3.** Satellite cell dysfunction in Duchenne muscular dystrophy. The left panel of the diagram gives an overview of the main cell types and developmental steps involved in regenerative myogenesis in normal adult skeletal muscles following an appropriate stimulus, such as injury to the multi-nucleated skeletal muscle fibre system. Hierarchical alterations in transcription factor expression patterns, including PAX7 (paired box 7), MYOD1 (myoblast determination protein 1) and MYOG (muscle-specific transcription factor myogenin), can be observed during cellular changes. The dormant muscle stem cell population consisting of non-activated satellite cells, which are located between the sarcolemma and basal lamina, is PAX7-positive and MYOD1/MYOG-negative. Cellular proliferation is based on a non-identical developmental path that replenishes the satellite cell pool via symmetric cell division and produces via asymmetric cell division myogenic progenitor cells, which are PAX7/MYOD1-positive and MYOG-negative. Cellular differentiation results in PAX7-negative and MYOD1/MYOG-positive myoblasts that fuse to form multi-nucleated myotubes for efficient muscle repair. In contrast, the right panel of the diagram provides a pathophysiological scheme that outlines the potential mechanisms that underlie satellite cell dysfunction in dystrophinopathy. A variety of studies have shown that dystrophin-deficient stem cells undergo on the one hand increased symmetric cell division that causes a certain degree of satellite cell hyperplasia, and on the other hand are characterized by decreased asymmetric cell division which results in drastically lower levels of myogenic progenitor cells. The loss of stem cell polarization appears to be related to abnormal interactions between the greatly reduced levels of dystrophin Dp427-M, the microtubule affinity regulating serine-threonine kinase MARK2 and the partitioning defective protein PARD3 (partitioning defective protein 3). This type of satellite cell dysregulation is postulated to play a key role in the diminished regenerative capacity of skeletal muscles in Duchenne patients.

including the important class of fibro-adipogenic progenitors (FAPs).<sup>70-72</sup> The FAPs type of cells participates in the generation of fibroblasts, myofibroblasts and adipocytes following activation by myofibre disintegration.<sup>73</sup> Prolonged periods of myofibre damage are associated with the shedding of characteristic

components of damage-associated molecular patterns (DAMPs) including ATP and nucleic acids.<sup>74</sup> The innate immune system recognizes DAMP molecules and triggers an inflammatory response involving nuclear factor NF- $\kappa$ B and the inflammasome.<sup>20</sup> Peptides or protein fragments frequently leak through the damaged

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and dystrophin-deficient sarcolemma. These muscle-derived molecules may act as neo-antigens in the body and can be recognized by the adaptive immune system, causing additional immunological reactions.<sup>60</sup>

**Reactive myofibrosis and fat replacement**

Chronic inflammation and reactive fibrosis appear to be closely linked in damaged myofibres, whereby the innate immune response was shown to be involved in the recruitment of large numbers of myofibroblasts.<sup>75</sup> Myofibroblasts are of central importance for fibrotic changes due to their enhanced synthetic capacity for the production of matrisomal proteins in muscular dystrophy.<sup>76</sup> Elevated levels of extracellular matrix protein secretion trigger endomysial fibrosis,<sup>77</sup> which is characterized by classical histopathological features of dystrophic muscles, including fibro-fatty scars that surround myofibres and thereby inhibit proper mechano-transduction processes.<sup>58,78</sup>

Skeletal muscle scarring and a general loss of tissue elasticity due to reactive myofibrosis are characteristic signs of dystrophinopathy.<sup>21</sup> The aged *mdx-4cv* mouse diaphragm muscle has been extensively surveyed as a highly suitable surrogate for studying reactive myofibrosis in X-linked muscular dystrophy using extracellular matrix proteomics.<sup>79</sup> As listed in Figure 2, major pathobiochemical features of myofibrosis include a drastic increase in collagen deposition and crosslinking, as well as the enhanced production of diverse matrisomal proteins. Elevated levels were established for the matricellular protein periostin, the repair proteins annexin-2 and annexin-6, nidogen, fibronectin, dermatopontin, vitronectin, the small leucine-rich proteoglycans asporin, biglycan, decorin, lumican and mimecan, as well as various collagens, including COL-IV, COL-VI, COL-XV and COL-XVIII.<sup>21,57,80</sup> This makes fibrosis an important therapeutic target in muscular dystrophy,<sup>81</sup> as outlined in below section on treatment strategies to counteract dystrophic symptoms. Of note, adipogenic precursors appear to participate in interstitial remodelling in muscular dystrophy resulting in aberrant adipogenesis. This process might play a role in linking myofibrosis to fat substitution in dystrophic muscles.<sup>82</sup> Increased fat replacement is associated with alterations in physiological cross-sectional muscle area and myofibre length,<sup>83,84</sup> resulting in abnormal contractile functions and metabolic disturbances.<sup>85</sup>

**Satellite cell dysfunction**

As summarized in Figure 2, stem cell dysfunction plays a crucial part in the dystrophic pathogenesis and involves the disruption of cellular polarity, the loss of asymmetric cell division and a reduction in properly activated myogenic progenitor cells.<sup>15,86</sup> In contrast to multi-nucleated and large sized myofibres, muscle stem cells (MuSCs) are a small, mono-nucleated and multi-potent cell type that is positioned between the sarcolemma and basal lamina of mature skeletal muscle fibres.<sup>6-8</sup> The pool

of available MuSCs is provided by a highly regulated process of self-renewal,<sup>7</sup> and combined with the essential creation of myogenic progenitor cells,<sup>8</sup> for repair and regeneration of adult myofibres.<sup>14</sup>

Figure 3 outlines the main steps involved in regenerative myogenesis. The presence of major myogenic factors, such as PAX7 (paired box 7),<sup>87</sup> MYOD1 (myoblast determination protein 1),<sup>88</sup> and MYOG (muscle-specific transcription factor myogenin),<sup>89</sup> are reliable markers of the various cell types,<sup>90</sup> that are involved in the regeneration of adult myofibres.<sup>91</sup> MYOG signalling is intrinsically involved in SC homeostasis and myocyte fusion.<sup>92</sup> While adult multi-nucleated skeletal muscle fibres are negative for PAX7, MYOD1 and MYOG, mono-nucleated myogenic precursor cells in their quiescent state are PAX7-positive. Myogenic progenitor cells produced by asymmetric division are PAX7/MYOD1-positive, but MYOG-negative. Following differentiation, these cells become PAX7-negative and MYOD1/MYOG-positive. The integration of signals that originate from the muscle environment trigger distinct changes in gene expression patterns based on complex epigenetic mechanisms, including nucleosome repositioning and post-translational modifications of chromatin.<sup>93</sup> Cellular fusion produces multi-nucleated myotubes, which then form regenerated myofibres by terminal differentiation.

The various cellular conversions can be conveniently followed by hierarchical alterations in transcription factor expression, including the general and not muscle-specific transcription factor FOXO (forkhead box O). Stem cell activation includes the following protein expression changes from quiescent SCs (positive for PAX7 and FOXO; but negative for MYF5, MYOD1 and MYOG) to activated SCs (positive for PAX7, MYF5 and MYOD1; but negative for FOXO and MYOG) to myoblasts (positive for PAX7, MYF5 and MYOD1; but negative for FOXO and MYOG) to myocytes (positive for MYOD1 and MYOG; but negative for PAX7, FOXO and MYF5). Therefore, patho-physiological scenarios with abnormal functioning of MuSCs in neuromuscular disease,<sup>1</sup> and/or diminished rates of stem cell differentiation are critical.<sup>94</sup> This can involve skeletal muscle precursor cells and their biological roles in a large variety of cellular processes, such as self-repair of damaged skeletal muscle fibres in association with muscle diseases, traumatic injury and neuromuscular aging,<sup>9-11</sup> as well as the maintenance of cellular homeostasis, muscle adaptations to changed contraction patterns and myofibre regeneration.<sup>95-98</sup>

Since stem cell dysfunction and regenerative exhaustion was shown to play a central role in X-linked muscular dystrophy,<sup>99</sup> mayor studies with a focus on SC abnormalities in dystrophin-deficient muscles are listed in Table 1.<sup>16-19,57,100-122</sup> Some of the contradictory findings on changes in SC numbers in dystrophic muscles from Duchenne patients and animal models of dystrophinopathy may be due to methodological

**Table 1.** List of major studies focusing on satellite cell and myogenic precursor cell dysfunction in dystrophinopathy.

| Bioanalytical approach  | Skeletal muscle specimens   | Characterization of skeletal muscle cells   | References   |
|---|---|---|--|
| Quantitative cell biological and ultrastructural analysis of SCs from dystrophic patients | Various muscle samples from patients ranging from preclinical to advanced stages of Duchenne muscular dystrophy   | Increased number of SCs in dystrophin-deficient myofibre populations; type I fibres exhibit higher numbers of PAX7-positive SCs as compared to type II fibres   | Wakayama et al., <sup>100</sup> ; Ishimoto et al., <sup>101</sup> ; Watkins and Cullen, <sup>102,103</sup> ; Kottlors and Kirschner, <sup>104</sup> ; Bankolé et al., <sup>105</sup> |
| Replicative life-span analysis of SCs from dystrophic patients                            | Isolated SCs of muscle specimens from 2-7 year old Duchenne patients  | Age-related decline in replicative capacity of isolated and dystrophin-deficient SCs  | Webster and Blau, <sup>106</sup>   |
| Evaluation of regenerative capacity in dystrophic muscles                                 | Primary cultures, isolated myofibres, 3-month old <i>extensor digitorum longus</i> and 6-month old diaphragm of <i>mdx-23</i> mouse                             | Demonstration of latent regenerative capacity in dystrophic muscles   | Yablonka-Reuveni and Anderson, <sup>16</sup> ; Boldrin et al., <sup>107</sup> ; Matecki et al., <sup>108</sup>   |
| Histological, biochemical and molecular biological analysis of SCs in dystrophic muscles  | <i>Gastrocnemius</i> from 3-month old <i>mdx-23</i> mouse, as compared to <i>DMD<sup>mdx</sup>/Large<sup>myd</sup></i> double mutant                            | Retention of PAX7-positive SC pool and proliferative capacity, but incomplete myofiber maturation and lack of preventing muscle degeneration  | Ribeiro et al., <sup>18</sup>  |
| Analysis of Notch signaling in SCs  | Myofiber preparations from <i>extensor digitorum longus</i> of 2-month old <i>mdx-23</i> mice   | Increased SCs in young <i>mdx-23</i> mice, followed by age-related decrease in SCs and Notch signalling deficiency  | Jiang et al., <sup>109</sup>   |
| Comparative analysis of SCs in <i>mdx-23</i> versus <i>mdx/utrophin</i> -/- dKO mice      | <i>Extensor digitorum longus</i> from 2-month old mouse models  | Depletion of SCs in severely dystrophic dKO mice, as compared to milder <i>mdx-23</i> phenotype   | Lu et al., <sup>110</sup>  |
| Cell biological analysis of dystrophin in SCs   | <i>Tibialis anterior</i> , <i>soleus</i> and <i>extensor digitorum longus</i> from mature Wistar rats   | Presence of dystrophin isoform Dp427-M in normal SCs  | Zhang and McLennan, <sup>111</sup>   |
| Analysis of epigenetic activation of SCs commitment in dystrophin-deficient muscles       | <i>Tibialis anterior</i> and <i>extensor digitorum longus</i> from 2-month old <i>mdx-23</i> mice   | Asymmetric division of SCs involves MYF5 activation by PAX7, depending on CARM1, a specific substrate of p38 $\gamma$ /MAPK12. Dysregulation of p38 $\gamma$ /CARM1 signaling occurs in <i>mdx-23</i> muscles | Chang et al., <sup>112</sup>   |
| Cell biological analysis of dystrophin in dystrophic muscles                              | <i>Tibialis anterior</i> from 3-month old <i>mdx-23</i> mouse   | Demonstration of association of dystrophin deficiency with decrease in the cell polarity regulators MARK2 and PARD3   | Dumont et al., <sup>17</sup>   |
| Transcriptomic analysis of <i>mdx</i> myoblasts   | <i>Gastrocnemius</i> -derived myoblasts from 2-month old <i>mdx-23</i> and <i>mdx-<math>\beta</math>geo</i> mice, and Duchenne patient myoblasts                | Significant alteration of gene expression including <i>MyoD</i> , <i>MyoG</i> , <i>Mymk</i> and <i>Mymx</i> , resulting in increased myoblast proliferation.  | Gosselin et al., <sup>113</sup>  |
| Proteomic screening of total muscle extracts  | Diaphragm, 3-month versus 15-month old <i>mdx-4cv</i> mouse   | Increase in myogenic marker CD34  | Gargan et al., <sup>57</sup>   |
| Multi-omics analysis of myogenesis in dystrophinopathy                                    | Human tissue-derived myoblasts and human induced pluripotent stem cells from Duchenne patients  | Establishment of early developmental manifestation of the dystrophic phenotype during myogenesis  | Mournetas et al., <sup>114</sup>   |
| Molecular biological and physiological characterization of <i>mdx-23</i> myoblasts        | Immortalized <i>mdx-23</i> and dystrophin-positive control myoblast cell lines, and primary myoblasts from 2-month old <i>mdx-23</i> hindlimb muscles           | Myoblasts from <i>mdx-23</i> muscle exhibit abnormal calcium-signaling and increased susceptibility to purinergic receptor P2Y-mediated stimulation, causing reduced myoblast motility                        | Róg et al., <sup>115,116</sup>   |
| Modelling of dystrophic patient-specific phenotypes in reprogrammed myotubes              | Bioengineered dystrophic muscle tissues using culturing and differentiating of MYOD1-directly reprogrammed fibroblasts from Duchenne patients                   | Determination of cellular and molecular pathogenesis and mechanisms of regeneration in dystrophic myotubes  | Barthélémy et al., <sup>19</sup>   |
| Analysis of dystrophic patient-derived human induced pluripotent stem cells               | Skeletal myotubes generated from hiPSCs from 1-8 year old Duchenne patients   | Demonstration of pronounced calcium influx in myotubes following electric stimulation for <i>in vitro</i> contraction; evaluation of therapeutic strategies   | Shoji et al., <sup>117</sup> ; Yoshioka et al., <sup>118</sup>   |
| Analysis of disturbed bioenergetic metabolism in dystrophic myoblasts                     | Immortalized <i>mdx-23</i> mouse myoblasts and dystrophin-positive controls; <i>extensor digitorum longus</i> from 2-month old <i>mdx/utrophin</i> -/- dKO mice | Mitochondrial dysfunction in dystrophic myoblasts and fused myofibres is associated with reduced oxygen consumption, altered mitochondrial membrane potential and high levels of reactive oxygen species      | Onopiuk et al., <sup>119</sup> ; Pant et al., <sup>120</sup> ; Matre et al., <sup>121</sup>  |
| Analysis of SCs senescence in muscular dystrophy  | <i>Tibialis anterior</i> and diaphragm primary cell preparations from the dystrophic rat model (DMD rat)  | Cellular senescence-mediated exacerbation of muscular dystrophy in association with increased expression of senescence marker genes <i>CDKN2A</i> , <i>p16</i> and <i>p19</i>                                 | Sugihara et al., <sup>122</sup>  |

differences in counting approaches and data normalisation in relation to myofibres, myonuclei or muscle area, as recently discussed by Morgan and Partridge.<sup>123,124</sup> Most studies suggest that dystrophin-deficient muscle fibre populations exhibit some degree of SC hyperplasia.<sup>100-104</sup> Increased numbers of PAX7-positive and Dp427-lacking SCs were especially observed in slow-twitching type I fibres as compared to faster twitching type II fibres.<sup>105</sup> However, an age-related decline in replicative capacity of isolated and dystrophic SCs was shown to occur in

young Duchenne patients.<sup>106</sup> Increased SC levels are clearly present in young *mdx-23* mice, which is followed by an age-related decrease in SCs and abnormal Notch signalling,<sup>109</sup> which is a crucial pathway in muscle stem cell development.<sup>125</sup> Notably, depletion of SCs was observed in the severely dystrophic *mdx/utrophin*-/- dKO mouse model of dystrophinopathy, as compared to the milder *mdx-23* phenotype.<sup>110</sup>

Latent regenerative capacity in dystrophic muscles,<sup>16,107,108</sup> is characterized by the retention of a stem cell pool of PAX7-positive SCs with proliferative

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capacity, but incomplete myofiber maturation and lack of preventing skeletal muscle degeneration.<sup>18</sup> Thus, a major pathobiological concept of MuSCs dysfunction in dystrophinopathy is based on the assumption that a disrupted balance of activated SCs exists between symmetric cell division, which is involved in the self-renewal of SCs, and asymmetric cell division, which produces myogenic precursor cells for muscle repair, as diagrammatically outlined in Figure 3.<sup>15</sup> The membrane cytoskeletal protein dystrophin is positioned in the subsarcolemmal region in mature myofibres,<sup>126</sup> but also present at relatively high abundance in activated MuSCs and was shown to play a regulatory role in SC polarity and the support of asymmetric cell division.<sup>17,111</sup>

In dystrophin-containing normal SCs, Dp427-M interacts with  $\beta$ 1-syntrophin, which in turn binds to the mitogen-activated protein kinase p38 $\gamma$ /MAPK12, and a key regulator of cell polarity, the microtubule affinity regulating serine-threonine kinase MARK2 (PAR1b).<sup>17,59,94</sup> Symmetric division of SCs involves MYF5 (myogenic factor 5) activation by PAX7, depending on CARM1 (coactivator-associated arginine methyltransferase 1), a specific substrate of p38 $\gamma$ /MAPK12. Importantly, the uneven distribution of dystrophin is essential for supporting asymmetric cell division and the initiation of myogenic differentiation in normal skeletal muscle SCs. In contrast, MARK2 expression levels are reduced in dystrophin-lacking SCs, which inhibits the proper delocalization of the cell polarity regulator PARD3 (partitioning defective protein 3) to the opposing side of SCs.<sup>17</sup>

Dysregulation of p38 $\gamma$ /CARM1 signalling occurs in *mdx-23* muscles.<sup>112</sup> Hence, the reduction of asymmetric divisions of SCs that lack dystrophin leads to a drastically lower numbers of myogenic progenitors, which are essential for fibre regeneration. This diminished regenerative capacity due to SC dysfunction in association with Dp427-MARK2-PARD3 dysregulation and a loss of cell polarization,<sup>17</sup> decisively intensifies the overall pathogenesis of dystrophinopathy, which is characterized by highly progressive myonecrosis, chronic inflammation, fat substitution and reactive myofibrosis.

Besides altered patterns of cell division, dystrophic SCs and their activated cell progeny were also shown to be associated with abnormal cellular signalling, metabolic disturbances, defective epigenetic mechanisms, disturbed calcium signalling and mitochondrial dysfunction.<sup>94</sup> Dystrophic myoblasts and fused myofibres exhibit mitochondrial abnormalities, including reduced oxygen consumption, altered mitochondrial membrane potential and high levels of reactive oxygen species.<sup>119-121</sup> Myoblasts from *mdx-23* muscle are characterized by abnormal Ca<sup>2+</sup>-signalling and an increased susceptibility to purinergic receptor P2Y-mediated stimulation, causing reduced myoblast motility.<sup>115,116</sup> Studies with dystrophic myotubes have revealed abnormal signalling patterns and considerable

Ca<sup>2+</sup>-influx into myocytes following electric stimulation, which can be used as an experimental system for the evaluation of novel therapeutic strategies.<sup>19,117,118</sup> Cellular senescence-mediated exacerbation of muscular dystrophy was established to occur in association with increased expression of senescence marker genes such as *CDKN2A*, *p16* and *p19*.<sup>122</sup> Thus, the inherited muscle wasting disorder DMD fits into the general category of secondarily affected satellite cellopathies.<sup>1,127</sup>

**Satellite cells in protected extraocular muscles**

In contrast to most skeletal muscle types in the body and their susceptibility to inherited disorders, a divergent subtype is represented by extraocular muscles (EOM) with their unusually high presence of activated stem cells and accompanying levels of extraordinary regenerative capacity.<sup>128</sup> The study of SCs in the EOM cell niche is therefore of considerable biomedical importance, since they represent a naturally protective phenotype of muscular dystrophy.<sup>129</sup> Despite dystrophin deficiency, EOMs retain efficient regenerative capacity.<sup>130,131</sup> A high proliferative rate of specialized regenerative myogenic precursor cell populations seems to play a key role in this protection of EOM morphology and physiological function.<sup>132,133</sup>

EOMs are characterized by a high degree of PITX2 (paired-like homeodomain transcription factor 2) - positive myogenic precursor cells, whereby this transcription factor is involved in the regulation of SC differentiation.<sup>134</sup> Biochemical and proteomic studies confirmed the mild phenotype of dystrophin-lacking EOMs,<sup>135-137</sup> and showed the compensatory upregulation and extra-junctional localization of the autosomal dystrophin homologue utrophin,<sup>138,139</sup> which is highly enriched at the neuromuscular junction in normal skeletal muscle fibres.<sup>140</sup> Hence, the small size of EOMs with relatively low load bearing, a highly efficient Ca<sup>2+</sup>-extrusion system, extra-junctional utrophin expression and associated rescue of sarcolemmal glycoproteins and/or a significantly higher level of regenerative capacity could explain the milder dystrophic phenotype of this highly specialized type of skeletal muscles.<sup>129,132,141</sup>

**Proteomics of satellite cell dysfunction**

Although only a limited number of omics-type studies have so far directly focused on the detailed characterization of SCs,<sup>142-144</sup> or the specific role of SCs in dystrophinopathy,<sup>57,113,114</sup> high-throughput systems biological approaches have great potential to further elucidate the role of SC modulation and dysfunction in health and disease. The transcriptomic analysis of *mdx-23* myoblasts has established significant alterations in gene expression patterns, including *MyoD*, *MyoG*, *Mymk* and *Mymx*, indicating increased myoblast proliferation.<sup>113</sup> The proteomic screening of total muscle extracts of 3-month versus 15-month old *mdx-4cv* mouse diaphragm preparations has revealed increased levels of



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the putative myogenic markers CD34 and cadherin-13 (CDH13, T/H-cadherin).<sup>57</sup> The surface marker protein CD34 was previously identified as a robust SC-linked biomarker.<sup>145-147</sup> A multi-omics analysis of dystrophinopathy was carried out with human tissue-derived myoblasts and human induced pluripotent stem cells (hiPSCs) from Duchenne patients, and established the early developmental manifestation of the dystrophic phenotype during myogenesis.<sup>114</sup>

These initial findings highlight the enormous potential of future proteomics-based studies for the detailed characterization of protein alterations in SCs, focusing specifically on single cell proteomics (SCP).<sup>148-150</sup> Technological approaches using high-throughput sequencing of DNA and RNA in individual cells have contributed enormously to the omics field to date. Proteomic profiling is currently lagging behind these advanced molecular biological screening methods in terms of sensitivity and coverage.<sup>151</sup> However, advancements in the ability to perform SCP is now on a significant upwards trajectory, due in no small part to innovations in sample preparation, chromatography, mass spectrometry hardware and associated workflows.<sup>152</sup> Isobaric tag-based workflows allow for 1000-1500 protein groups to be quantified per cell, with the ability to run dozens of samples daily, demonstrating the high-throughput nature of this approach.<sup>153</sup> Using specific isobaric tandem mass tags (TMT) to label peptides originating from a single cell, multiplexing employing the latest reagents allows multiple individual samples to be combined, often including a carrier channel (100-200 cells) to facilitate peptide identification.<sup>154</sup>

Label-free quantification (LFQ) workflows evaluate each single cell sample individually, with approximately 2000 protein groups identifiable using data dependent acquisition (DDA) modes.<sup>155</sup> However, this approach is more time consuming, reducing the daily number of samples that can be analysed. Many of the studies reporting on SCP and numbers of identifiable protein groups focus on cell lines, for example HeLa cells.<sup>156</sup> Of note, isolated individual muscle fibres contain significantly higher concentrations of protein than HeLa cells, potentially increasing the capability of applying a SCP approach to fragment and identify protein species associated with the myocyte phenotype.<sup>157-159</sup> Recently, Momenzadeh and co-workers,<sup>160</sup> demonstrated the bioanalytical usefulness of this powerful approach, using 15 min run times on a Bruker Tims-TOF SCP instrument combining parallel accumulation serial fragmentation (PASEF) with a data-independent acquisition (DIA) approach, called diaPASEF. Comparing type 1 and 2a myofibres, 94 proteins were found to be statistically different between clusters. This demonstrates the power of this proteomic approach and future applications in muscle physiology and pathophysiology, including muscle regeneration,<sup>161</sup> and the evaluation of novel therapeutic strategies such as myoblast transfer therapy to treat dystrophinopathy.<sup>162</sup>

**Therapeutic approaches**

Based on the description of major aspects of the molecular and cellular pathogenesis of DMD, a brief overview of novel therapeutic approaches to treat the complex and multi-systems abnormalities of dystrophinopathy is given. A more detailed discussion of impending improvements in pharmacotherapy, stem cell therapy and gene editing is beyond the scope of this review that has focused on muscle degeneration due to dystrophin deficiency. However, a large number of excellent and comprehensive reviews on DMD treatment options have recently been published.<sup>35-37,163</sup> Reports on advances with preclinical and clinical trials and critical discussions of potential issues with biomedical and technical limitations, as well as the clinical advantages of diverse pharmacological, cellular and genetic approaches are available.<sup>38,164-166</sup> The major categories of therapeutic approaches can be divided into (i) muscle stem cell therapy,<sup>167-174</sup> (ii) the pharmacological treatment of complex symptoms associated with the cardio-respiratory syndrome, disturbed ion handling, abnormal cellular signalling, chronic inflammation, disturbed bioenergetics, abnormal cellular growth, dysregulated metabolism and chronic oxidative stress,<sup>175-180</sup> using potentially multi-drug combinations tested in suitable dystrophic animal models,<sup>181</sup> (iii) exon-skipping therapy using antisense molecules,<sup>37,182-187</sup> (iv) CRISPR/Cas9 (clustered regularly interspaced short palindromic repeats and CRISPR-associated protein 9) - mediated exon excision and somatic genome editing,<sup>36,188-190</sup> (v) stop codon read-through therapy,<sup>191,192</sup> (vi) vector transfer therapy,<sup>193-195</sup> (vii) targeted dystrophin substitution via its autosomal homologue utrophin,<sup>196-198</sup> (viii) up-regulation of distinct molecular chaperones, such as heat shock proteins, to strengthen the cellular stress response,<sup>199,200</sup> and (ix) electro-stimulation therapy to trigger muscle transformation.<sup>201</sup>

In response to chronic myonecrosis and inflammation, dystrophic skeletal muscles undergo considerable changes in their extracellular matrix environment. Since tissue scarring due to reactive myofibrosis plays a central role in the loss of muscle tissue elasticity and contractility,<sup>78</sup> as well as representing a barrier to many therapeutic approaches including stem cell therapy and gene transfer,<sup>202</sup> anti-fibrosis therapy is of crucial importance in the field of DMD treatment.<sup>81</sup> A drastic decrease in pro-fibrotic proteins using exon-skipping therapy has been suggested as a suitable option to reduce excess scarring of dystrophic muscle tissues.<sup>203</sup>

In conclusion, DMD is characterized by SC dysfunction. Although dystrophin deficiency appears to cause initially SC hyperplasia, myogenic differentiation and muscle regeneration is impaired. A potential mechanism for triggering decreased levels of asymmetric divisions of dystrophic SCs is the reduced expression of crucial binding partners of dystrophin that result in loss of SC polarity. This gives stem cell therapy a central place in

novel treatment options for improving the regenerative capacity of dystrophic myofibres.

### List of acronyms

CARM1 - coactivator-associated arginine methyltransferase 1  
 COL - collagen  
 DAMP - damage-associated molecular patterns  
 DDA - data dependent acquisition  
 DIA - data-independent acquisition  
 dKO - double knockout  
 DMD - Duchenne muscular dystrophy  
 Dp - dystrophin protein  
 EOM - extraocular muscle  
 FAPs - fibro-adipogenic progenitors  
 FOXO - forkhead box O  
 hiPSCs - human induced pluripotent stem cells  
 LFQ - label-free quantification  
 MAPK12 - mitogen-activated protein kinase 12  
 MARK2 - microtubule affinity regulating kinase 2  
 MuSCs - muscle stem cells  
 MYF5 - myogenic factor 5  
 MYOD1 - myoblast determination protein 1  
 MYOG - muscle-specific transcription factor myogenin  
 P2Y - purinoceptor 2  
 PARD3 - partitioning defective protein 3  
 PASEF - parallel accumulation serial fragmentation  
 PAX7 - paired box 7 transcription factor  
 PITX2 - paired-like homeodomain transcription factor 2  
 SC - satellite cell  
 SCP - single cell proteomics  
 TGF - transforming growth factor  
 TMT - tandem mass tags  
 TNF - tumour necrosis factor

### Contributions of Authors

PD, DS, and KO were involved in the conceptualization and initiation of this review project, as well as the design of the literature search strategy. All authors were involved in the writing and final editing of the typescript. All authors read and approved the final edited typescript.

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The authors declare no competing interests.

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